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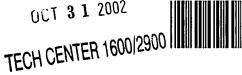
UNITED STATES DEPARTMENT OF COMMERCE United State: Patent and Trademark Office Address: COMMISSIONER OF PATENTS AND TRADEMARKS Washington, D.C. 20231 www.uspto.gov

CONFIRMATION NO. FIRST NAMED INVENTOR ATTORNEY DOCKET NO. FILING DATE APPLICATION NO. 2254-031 2896 Vered Hornik 09/644,456 11/04/2002 28765 7590 EXAMINER **WINSTON & STRAWN** PATENT DEPARTMENT BORIN, MICHAEL L 1400 L STREET, N.W. WASHINGTON, DC 20005-3502 ART UNIT PAPER NUMBER 1631 DATE MAILED: 11/04/2002

Please find below and/or attached an Office communication concerning this application or proceeding.



OCT 3 1 2002





1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/644,456A

DATE: 10/24/2002

TIME: 14:30:37

Input Set : A:\#724253 v1 - sequence listing text.txt

Output Set: N:\CRF4\10242002\1644456A.raw

4 <110> APPLICANT: HORNIK, V. and HADAS, E.

6 <120> TITLE OF INVENTION: CONFORMATIONALLY CONSTRAINED BACKBONE

CYCLIZED INTERLEUKIN-6 ANTAGONISTS

9 <130> FILE REFERENCE: 87534-3100

11 <140> CURRENT APPLICATION NUMBER: US 09/644,456A

12 <141> CURRENT FILING DATE: 2000-08-024

E--> 14 <160> NUMBER OF SEQ ID NOS: (82) 83 (see Lebow)
16 <170> SOFTWARE: FastSEQ for Windows Version 4.0

Does Not Comply Corrected Diskette Needed

ERRORED SEQUENCES

last sequere in submitted file 756 <210> SEQ ID NO: 83

757 <211> LENGTH: 6

758 <212> TYPE: PRT

759 <213> ORGANISM: homo sapiens

761 <220> FEATURE:

762 <221> NAME/KEY: misc_feature

763 <222> LOCATION: (4) .. (4)

764 <223> OTHER INFORMATION: ornithine

766 <400> SEQUENCE: 83

W--> 767 Lys Lys Ala Xaa Trp Phe E--> 768 1 (5) Smisaliged arrivo acid humbers 776 NY:724253.1 (see item 3 on Eva Summary Sheet)





DATE: 10/24/2002 VERIFICATION SUMMARY TIME: 14:30:39 PATENT APPLICATION: US/09/644,456A

Input Set : A:\#724253 v1 - sequence listing text.txt

Output Set: N:\CRF4\10242002\I644456A.raw

L:12 M:256 W: Invalid Numeric Header Field, Wrong Current FILING DATE:YYYY-MM-DD

L:767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83 after pos.:0 L:768 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:83

L:14 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (82) Counted (83)



ERROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: 09/644,456A
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE	
1Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001